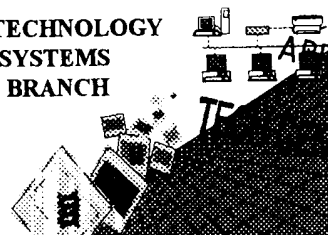


## **RAW SEQUENCE LISTING** **ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



RECEIVED

01 2003

TECHNICAL CENTER 1600/2900

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 07/674,436A  
Source: 1600  
Date Processed by STIC: 5/27/03

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

# Raw Sequence Listing Error Summary

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APR 01 2000  
TECH CENTER 1600/2900

**ERROR DETECTED**      **SUGGESTED CORRECTION**      **SERIAL NUMBER:** 001001-1001

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

- 1      Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length      Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    This sequence is intentionally skipped  
  
    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
    <210> sequence id number  
    <400> sequence id number  
    000
- 9      Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>      Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
    (See "Federal Register," 06/01/1998, Vol 63, No 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n      n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



1600

## RAW SEQUENCE LISTING

DATE: 03/27/2003

PATENT APPLICATION: US/09/674,436A

TIME: 10:49:21

Input Set : A:\09674436 Sub Seq List.txt

Output Set: N:\CRF4\03272003\I674436A.raw

```

3 <110> APPLICANT: Kotaki, Toyomi
4      Tsukada, Masahiro
5      Suzuki, Koichi
6      Yang, Ping
7 <120> TITLE OF INVENTION: Gene Any-RE Dormancy Control Substance and Method for
Preparing the Same
8      as Well As Cell Control Agent
9 <130> FILE REFERENCE: 04656-00004
10 <140> CURRENT APPLICATION NUMBER: US 09/674,436A
11 <141> CURRENT FILING DATE: 2001-07-16
12 <150> PRIOR APPLICATION NUMBER: PCT/JP00/03388
13 <151> PRIOR FILING DATE: 2000-05-26
14 <160> NUMBER OF SEQ ID NOS: 4
15 <170> SOFTWARE: Microsoft WORD
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 5
18 <212> TYPE: PRT
19 <213> ORGANISM: Antheraea yamamai Guerin-Meneville
20 <400> SEQUENCE: 1
21 Asp Ile Leu Arg Gly
22      5
23 <210> SEQ ID NO: 2
24 <211> LENGTH: 4
25 <212> TYPE: PRT
26 <213> ORGANISM: prepared by peptide synthesis in a laboratory
27 <400> SEQUENCE: 2
28 Ile Leu Arg Gly
29 <210> SEQ ID NO: 3
30 <211> LENGTH: 7
31 <212> TYPE: PRT
32 <213> ORGANISM: prepared by peptide synthesis in a laboratory
W--> 46 <220> FEATURE:
W--> 47 <221> NAME/KEY: Acp
33 <222> LOCATION: 1
34 <223> OTHER INFORMATION: epsilon 6-aminocaproic acid
35 <224> NAME/KEY: Amidation
36 <225> LOCATION: 1
37 <226> OTHER INFORMATION: C-terminal amino acid amidated
W--> 54 <400> 3
W--> 55 Cys Xaa Asp Ile Leu Arg Gly
38      5
39 <210> SEQ ID NO: 4
40 <211> LENGTH: 4
41 <212> TYPE: PRT

```

## RAW SEQUENCE LISTING

DATE: 03/27/2003

PATENT APPLICATION: US/09/674,436A

TIME: 10:49:21

Input Set : A:\09674436 Sub Seq List.txt

Output Set: N:\CRF4\03272003\I674436A.raw

61 &lt;213&gt; ORGANISM: Prepared by peptide synthesis in a laboratory

## W--&gt; 62 &lt;220&gt; FEATURE:

63 &lt;221&gt; NAME/KEY: Amidation

64 &lt;222&gt; LOCATION: 4

65 &lt;223&gt; OTHER INFORMATION: C-terminal amino acid amidated

67 &lt;400&gt; SEQUENCE: 4

68 Phe Met Arg Phe

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/674,436A

DATE: 03/27/2003  
TIME: 10:49:22

Input Set : A:\09674436 Sub Seq List.txt  
Output Set: N:\CRF4\03272003\I674436A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:0; Xaa Pos. 2

## VERIFICATION SUMMARY

DATE: 03/27/2003

PATENT APPLICATION: US/09/674,436A

TIME: 10:49:22

Input Set : A:\09674436 Sub Seq List.txt

Output Set: N:\CRF4\03272003\I674436A.raw

L:46 M:283 W: Missing Blank Line separator, <220> field identifier  
L:47 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3  
L:54 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
L:55 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0  
L:62 M:283 W: Missing Blank Line separator, <220> field identifier